of composition 5'-B-TCC GGC GCG CCG TTT TCC CAG TCA CGA(30)-3' (SEQ ID NO:126), contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the strepavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

REMARKS

Attached hereto is a marked-up version of the changes made to the specification by current amendments. The attached page captioned "Version With Markings to Show Changes Made." No new matter has been added.

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, Applicants have not enclosed a Sequence Listing corresponding to the markers identified by a GenBank GI number. Applicants respectfully submit that Table 8A-1 contains GenBank GI numbers for each marker, which are incorporated by reference. As set forth in the specification on page 87, lines 17-22:

'GenBank Accession Number' or 'Accession No.' or 'acc' or 'Accession #' or 'Acc Num' is the identification number assigned to the marker in the relevant database (see, *e.g.* 'http://www.ncbi.nlm.nih.gov/genbank/query_form.html' and 'www.derwent.com' for further information). 'GI Nbr' or 'Nuc Seq Id #' is the GI identification number assigned to the marker in the GenBank database (see *supra*). All referenced database sequences are expressly incorporated herein by reference.

Applicants further submit that the sequence content corresponding to a GenBank GI identification number is fixed and cannot be altered by addition or correction. Therefore, Applicants have not enclosed a Sequence Listing in Response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures for the markers identified in Tables 1-13 that correspond to a GenBank GI number.

Applicants have enclosed a Sequence Listing (SEQ ID NOS:1-126) corresponding to the 125 sequences identified in Table 8B, which do not have an identified GenBank GI number. In addition, Applicants have identified the primer sequence in the specification at page 27, lines 33-34 as SEQ ID NO:126.

RESPONSE TO RESTRICTION REQUIREMENT

This is in response to the restriction requirement set forth in the Office Action dated October 15, 2002. The Examiner has required restriction to one of the following inventions under 35 U.S.C. § 121:

I. Claims 1-23 and 38, drawn to a method and kit for detecting cervical cancer or a pre-malignant condition, classified in class 436, subclass 64.

II. Claims 24-30, drawn to a method for monitoring the progression of cervical cancer or a pre-malignant condition, classified in class 436, subclass 64.

III. Claims 31-37, 39, and 46, drawn to a method and kit of assessing the efficacy of a therapy for inhibiting cervical cancer, classified in classes 514 and 600, subclasses 1 and 1, respectively.

IV. Claim 40, drawn to a method of making a hybridoma which produces an antibody, classified in class 436, subclass 547.

V. Claims 41 and 42, drawn to an antibody and kit, classified in class 530, subclass 387.1.

VI. Claims 43-44, drawn to a method and kit of assessing cervical cell carcinogenic potential of a test compound, classified in class 530, subclass 388.21.

VII. Claim 45, drawn to a treating a patient with cervical cancer, classified in class 514, subclass 44.

Applicants hereby elect the Group 1 invention **(Claims 1-23 and 38)** for prosecution in this application, *without traverse*. Applicants further elect **SEQ ID NO:100** for prosecution in the application.

Applicants reserve the right to traverse the restriction between the non-elected group in this or a separate application.

Dated: April 15, 2003

Respectfully submitted,

By _____

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Please insert after the last page of the specification, before the claims, the Sequence Listing submitted herewith, which contains SEQ ID NOS:1-126.

Replace the paragraph at page 27, line 29 through page 28, line 2 of the specification with the following paragraph,

> RNA from a source to express the cDNA corresponding to a given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to derive the first strand synthesis. For example, the oligonucleotide of composition 5'-B-TCC GGC GCG CCG TTT TCC CAG TCA CGA(30)-3' (SEQ ID NO:126), contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the strepavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.